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Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: [year=2008; month=11; day=6; hr=9; min=35; sec=23; ms=48; ]
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<223>   Promoter GAL 1 (pVP2)

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For all sequences using "Artificial sequence", for numeric identifier
<213>, a mandatory feature is required to explain the source of the
genetic material. The feature consists of <220>, which remains blank,
and <223>, which states the source of the genetic material. To explain
the source, if the sequence is put together from several organisms,
please list those organisms. If the sequence is made in the laboratory,
please indicate that the sequence is synthesized. These errors appear in
other sequences in the sequence listing. Please make all necessary
changes.

* *

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           Validated By CRFValidator v 1.0.3
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Application No: 10576988   Version No: 1.0

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                    Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 83 ms
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Error code   Error Description

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E   224   <220>,<223> section required as <213> has Artificial sequence or
               Unknown in SEQID (9)

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<110>   Rodriguez Aguirre et al.

<120>   EMPTY CAPSIDS (VLPs(-VP4)) OF THE INFECTIOUS BURSAL DISEASE VIRUS
(IBDV), OBTAINMENT PROCESS AND APPLICATIONS

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<150>   PCT/EP2005/000694
<151>   2005-01-21

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accatctcgc aaataaataa gtattttact gttttcgtaa cagttttgta ataaaaaaac   240

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Asn Leu Ser Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg Ser Leu
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Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr Leu Glu
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Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr Val Gly
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Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro Gly Ser
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Ile Val Gly Ala His Tyr Thr Leu Gln Gly Asn Gly Asn Tyr Lys Phe
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Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr Asn Tyr
         85   90   95

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Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr Leu Pro
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Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys Met Val
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Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro
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Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr
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Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr
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Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu
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Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val
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Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly
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Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys
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Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile
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Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly
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